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1. (Amended two times) A method of identifying a compound that binds to a coactivator binding site of a nuclear receptor, said method comprising:

modeling test compounds that fit spatially into the nuclear receptor coactivator binding site using an atomic structural model of the nuclear receptor coactivator binding site or portion thereof,

screening said test compounds in an assay that measures binding of a test compound to the nuclear receptor coactivator binding site, and

identifying a test compound that binds to the coactivator binding site of said nuclear receptor.

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2. (Amended once) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues of human thyroid receptor selected from the group consisting of Val284, Phe293, Ile302, Leu305, and Leu454.

3. (Amended once) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues of human thyroid receptor selected from the group consisting of Val284, Lys288, Ile302, Lys306, Leu454 and Glu457.

4. (Amended once) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues of human thyroid receptor helix 3 residues Ile280, Thr281, Val283, Val284, Ala287, and Lys288, helix 4 residue Phe293, helix 5 residues Gln301, Ile302, Leu305, Lys306, helix 6 residue Cys309, and helix 12 residues Pro453, Leu454, Glu457, Val458 and Phe459.

5. (Amended once) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues of human thyroid receptor selected from the group consisting of helix 3 residues Ile280, Thr281, Val283, Val284, Ala287, and Lys288, helix 4 residue Phe293, helix 5

residues Gln301, Ile302, Leu305, Lys306, helix 6 residue Cys309, and helix 12 residues Pro453, Leu454, Glu457, Val458 and Phe459.

6. (Amended once) The method of claim 5, wherein said amino acid residues identified by homology alignment with residues of human thyroid receptor comprise Val284, Phe293, Ile302, Leu305, and Leu454.

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7. (Amended once) The method of claim 5, wherein said amino acid residues identified by homology alignment with residues of human thyroid receptor comprise Val284, Lys288, Ile302, Lys306, Leu454 and Glu457.

8. (Amended once) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues of human thyroid receptor of helix 3 residues Ile280, Thr281, Val283, Val284, Ala287, and Lys288, helix 4 residue Phe293, helix 5 residues Gln301, Ile302, Leu305, Lys306, helix 6 residue Cys309, and helix 12 residues Pro453, Leu454, Glu457, Val458 and Phe459.

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12. (Amended once) The method of claim 1, wherein said assay is a *in vivo* assay.

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16. (Amended two times) The method of Claim 15, wherein the test compound is a peptide comprising a nuclear receptor box (NR-box) amino acid sequence or derivative thereof.

Please add new claim 31.

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31. (New) The method of Claim 1 wherein the atomic coordinates of the nuclear receptor coactivator binding site are provided to a computerized modeling system.